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ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/975,723A

DATE: 01/16/2003

TIME: 14:19:52

Input Set : A:\601-1-101N SEQUENCE LISTING.TXT

Output Set: N:\CRF4\01162003\I975723A.raw

4 <110> APPLICANT: Nackman, Gary
 5 Foty, Ramsey
 7 <120> TITLE OF INVENTION: Improvement of Endothelial Cell-Cell
 8 Cohesion
 10 <130> FILE REFERENCE: 601-1-101N
 12 <140> CURRENT APPLICATION NUMBER: 09/975,723A
 13 <141> CURRENT FILING DATE: 2001-10-11
 15 <150> PRIOR APPLICATION NUMBER: 60/241,216
 16 <151> PRIOR FILING DATE: 2000-10-13
 18 <150> PRIOR APPLICATION NUMBER: 60/243,693
 19 <151> PRIOR FILING DATE: 2000-10-27
 21 <160> NUMBER OF SEQ ID NOS: 2
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 829
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Homo sapiens
 30 <400> SEQUENCE: 1
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 32 1 5 10 15
 33 Cys Trp Leu Gln Cys Ala Ala Ser Glu Pro Cys Arg Ala Val Phe Arg
 34 20 25 30
 35 Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala Glu Gln Glu Pro Gly
 36 35 40 45
 37 Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala
 38 50 55 60
 39 Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr
 40 65 70 75 80
 41 Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe
 42 85 90 95
 43 Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala
 44 100 105 110
 45 Pro Ile Ser Val Pro Glu Asn Gly Lys Gly Pro Phe Pro Gln Arg Leu
 46 115 120 125
 47 Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser
 48 130 135 140
 49 Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val
 50 145 150 155 160
 51 Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys Pro Leu Asp Arg Glu
 52 165 170 175
 53 Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly
 54 180 185 190
 55 Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln

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56	195	200	205
57 Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val			
58 210	215	220	
59 Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr			
60 225	230	235	240
61 Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser			
62 245	250	255	
63 Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile			
64 260	265	270	
65 His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg			
66 275	280	285	
67 Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp			
68 290	295	300	
69 Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp			
70 305	310	315	320
71 Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His			
72 325	330	335	
73 Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr			
74 340	345	350	
75 Asp Leu Asp Ala Pro Asn Ser Pro Ala Trp Arg Ala Thr Tyr Leu Ile			
76 355	360	365	
77 Met Gly Gly Asp Asp Gly Asp His Phe Thr Ile Thr Thr His Pro Glu			
78 370	375	380	
79 Ser Asn Gln Gly Ile Leu Thr Thr Arg Lys Gly Leu Asp Phe Glu Ala			
80 385	390	395	400
81 Lys Asn Gln His Thr Leu Tyr Val Glu Val Thr Asn Glu Ala Pro Phe			
82 405	410	415	
83 Val Leu Lys Leu Pro Thr Ser Thr Ala Thr Ile Val Val His Val Glu			
84 420	425	430	
85 Asp Val Asn Glu Ala Pro Val Phe Val Pro Pro Ser Lys Val Val Glu			
86 435	440	445	
87 Val Gln Glu Gly Ile Pro Thr Gly Glu Pro Val Cys Val Tyr Thr Ala			
88 450	455	460	
89 Glu Asp Pro Asp Lys Glu Asn Gln Lys Ile Ser Tyr Arg Ile Leu Arg			
90 465	470	475	480
91 Asp Pro Ala Gly Trp Leu Ala Met Asp Pro Asp Ser Gly Gln Val Thr			
92 485	490	495	
93 Ala Val Gly Thr Leu Asp Arg Glu Asp Glu Gln Phe Val Arg Asn Asn			
94 500	505	510	
95 Ile Tyr Glu Val Met Val Leu Ala Met Asp Asn Gly Ser Pro Pro Thr			
96 515	520	525	
97 Thr Gly Thr Gly Thr Leu Leu Leu Thr Leu Ile Asp Val Asn Asp His			
98 530	535	540	
99 Gly Pro Val Pro Glu Pro Arg Gln Ile Thr Ile Cys Asn Gln Ser Pro			
100 545	550	555	560
101 Val Arg His Val Leu Asn Ile Thr Asp Lys Asp Leu Ser Pro His Thr			
102 565	570	575	
103 Ser Pro Phe Gln Ala Gln Leu Thr Asp Asp Ser Asp Ile Tyr Trp Thr			
104 580	585	590	

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105 Ala Glu Val Asn Glu Glu Gly Asp Thr Val Val Leu Ser Leu Lys Lys
106           595                      600                      605
107 Phe Leu Lys Gln Asp Thr Tyr Asp Val His Leu Ser Leu Ser Asp His
108           610                      615                      620
109 Gly Asn Lys Glu Gln Leu Thr Val Ile Arg Ala Thr Val Cys Asp Cys
110 625                      630                      635                      640
111 His Gly His Val Glu Thr Cys Pro Gly Pro Trp Lys Gly Gly Phe Ile
112           645                      650                      655
113 Leu Pro Val Leu Gly Ala Val Leu Ala Leu Leu Phe Leu Leu Leu Val
114           660                      665                      670
115 Leu Leu Leu Leu Val Arg Lys Lys Arg Lys Ile Lys Glu Pro Leu Leu
116           675                      680                      685
117 Leu Pro Glu Asp Asp Thr Arg Asp Asn Val Phe Tyr Tyr Gly Glu Glu
118 690                      695                      700
119 Gly Gly Gly Glu Glu Asp Gln Asp Tyr Asp Ile Thr Gln Leu His Arg
120 705                      710                      715                      720
121 Gly Leu Glu Ala Arg Pro Glu Val Val Leu Arg Asn Asp Val Ala Pro
122           725                      730                      735
123 Thr Ile Ile Pro Thr Pro Met Tyr Arg Pro Arg Pro Ala Asn Pro Asp
124           740                      745                      750
125 Glu Ile Gly Asn Phe Ile Ile Glu Asn Leu Lys Ala Ala Asn Thr Asp
126           755                      760                      765
127 Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly
128 770                      775                      780
129 Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser
130 785                      790                      795                      800
131 Asp Gln Asp Gln Asp Tyr Asp Tyr Leu Asn Glu Trp Gly Ser Arg Phe
132           805                      810                      815
133 Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu Asp Asp
134           820                      825

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137 <210> SEQ ID NO: 2

138 <211> LENGTH: 3170

139 <212> TYPE: DNA

140 <213> ORGANISM: Homo sapiens

142 <400> SEQUENCE: 2

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145 cctccgagcc gtgccgggcg gtcttcaggg aggctgaagt gaccttgag gcgggaggcg 180
146 cggagcagga gcccggccag gcgctgggga aagtattcat gggctgccct gggcaagagc 240
147 cagctctgtt tagcactgat aatgatgact tctctgtgcg gaatggcgag acagtccagg 300
148 aaagaaggte actgaaggaa aggaatccat tgaagatctt cccatccaaa cgtatcttac 360
149 gaagacacaa gagagattgg gtggttgctc caatatctgt ccctgaaaat ggcaagggtc 420
150 ccttccccca gagactgaat cagctcaagt ctaataaaga tagagacacc aagattttct 480
151 acagcatcac ggggccgggg gcagacagcc cccctgaggg tgtcttcgct gtagagaagg 540
152 agacaggctg gttgttggtg aataagccac tggaccggga ggagattgcc aagtatgagc 600
153 tctttggcca cgctgtgtca gagaatggtg cctcagtga ggaccccatg aacatctcca 660
154 tcatcgtgac cgaccagaat gaccacaagc ccaagtttac ccaggacacc ttccgaggga 720
155 gtgtcttaga gggagtccta ccaggtactt ctgtgatgca ggtgacagcc acagatgagg 780
156 atgatgccat ctacacctac aatgggggtg ttgcttactc catccatagc caagaaccaa 840

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157 aggacccaca cgacctcatg ttcacaattc accggagcac aggcaccatc agcgtcatct 900
158 ccagtggcct ggaccgggaa aaagtccctg agtacacact gaccatccag gccacagaca 960
159 tggatgggga cggctccacc accacggcag tggcagtagt ggagatcctt gatgccaatg 1020
160 acaatgctcc catgtttgac ccccagaagt acgaggccca tgtgcctgag aatgcagtgg 1080
161 gccatgaggt gcagaggctg acggtcactg atctggacgc ccccaactca ccagcgtggc 1140
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195 aagggtgagg acaatcgtgt atatgtacta gaactttttt attaaagaaa 3170
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